

SEQUENCE LISTING



<110> Sanders, Jane
Furmaniak, Jadwiga
Smith, Bernard Rees

<120> Binding Partners for the Thyrotropin Receptor and uses thereof

<130> URQU.P-016

<140> US 10/537,260
<141> 2003-11-28

<150> PCT/GB2003/005171
<151> 2003-11-28

<150> GB 0227964.4
<151> 2002-11-29

<150> GB 0302140.9
<151> 2003-01-29

<150> GB 0315147.9
<151> 2003-06-27

<160> 38

<170> PatentIn version 3.1

<210> 1
<211> 121
<212> PRT
<213> Homo sapiens

<400> 1

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Arg Gly Ser Gly Tyr Arg Phe Thr Ser Tyr
20 25 30

Trp Ile Asn Trp Val Arg Gln Leu Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Asp Pro Thr Asp Ser Tyr Thr Asn Tyr Ser Pro Ser Phe
50 55 60

Lys Gly His Val Thr Val Ser Ala Asp Lys Ser Ile Asn Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Gly Met Tyr Tyr Cys
85 90 95

Ala Arg Leu Glu Pro Gly Tyr Ser Ser Thr Trp Ser Val Asn Trp Gly

100

105

110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 2
 <211> 5
 <212> PRT
 <213> Homo sapiens

<400> 2

Ser Tyr Trp Ile Asn
 1 5

<210> 3
 <211> 17
 <212> PRT
 <213> Homo sapiens

<400> 3

Arg Ile Asp Pro Thr Asp Ser Tyr Thr Asn Tyr Ser Pro Ser Phe Lys
 1 5 10 15

Gly

<210> 4
 <211> 12
 <212> PRT
 <213> Homo sapiens

<400> 4

Leu Glu Pro Gly Tyr Ser Ser Thr Trp Ser Val Asn
 1 5 10

<210> 5
 <211> 131
 <212> PRT
 <213> Homo sapiens

<400> 5

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1 5 10 15

Ser Leu Lys Ile Ser Cys Arg Gly Ser Gly Tyr Arg Phe Thr Ser Tyr
 20 25 30

Trp Ile Asn Trp Val Arg Gln Leu Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45

Gly Arg Ile Asp Pro Thr Asp Ser Tyr Thr Asn Tyr Ser Pro Ser Phe
50 55 60

Lys Gly His Val Thr Val Ser Ala Asp Lys Ser Ile Asn Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Gly Met Tyr Tyr Cys
85 90 95

Ala Arg Leu Glu Pro Gly Tyr Ser Ser Thr Trp Ser Val Asn Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro
130

<210> 6
<211> 111
<212> PRT
<213> Homo sapiens

<400> 6

Leu Thr Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Arg Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Asn Ser Ser Asn Ile Gly Asn Asn
20 25 30

Ala Val Asn Trp Tyr Gln Gln Leu Pro Gly Lys Ala Pro Lys Leu Leu
35 40 45

Ile Tyr Tyr Asp Asp Gln Leu Pro Ser Gly Val Ser Asp Arg Phe Ser
50 55 60

Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Arg Gly Leu Gln
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Thr Ser Trp Asp Asp Ser Leu
85 90 95

Asp Ser Gln Leu Phe Gly Gly Gly Thr Arg Leu Thr Val Leu Gly
100 105 110

<210> 7
<211> 13
<212> PRT
<213> Homo sapiens

<400> 7

Ser Gly Asn Ser Ser Asn Ile Gly Asn Asn Ala Val Asn
1 5 10

<210> 8

<211> 7

<212> PRT

<213> Homo sapiens

<400> 8

Tyr Asp Asp Gln Leu Pro Ser
1 5

<210> 9

<211> 11

<212> PRT

<213> Homo sapiens

<400> 9

Thr Ser Trp Asp Asp Ser Leu Asp Ser Gln Leu
1 5 10

<210> 10

<211> 363

<212> DNA

<213> Homo sapiens

<400> 10

caaatgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccgggggagtc tctgaagatc 60
tcctgtaggg gttctggata cagggtttacc agctactgga tcaactgggt gcgccagctg 120
cccgggaaag gcctagagtg gatgggcagg attgatccta ctgactctta taccaactac 180
agtccatcct tcaaaggcca cgtcaccgtc tcagctgaca agtccatcaa cactgcctac 240
ctgcagtgga gcagcctgaa ggcctcggac accggcatgt attactgtgc gaggctcgaa 300
ccgggctata gcagcacctg gtccgtaa at tggggccagg gaaccctggc caccgtctcc 360
tca 363

<210> 11

<211> 15

<212> DNA

<213> Homo sapiens

<400> 11

agctactgga tcaac 15

<210> 12

<211> 51

<212> DNA

<213> Homo sapiens

<400> 12
 aggattgata ctactgactc ttataccaac tacagtccat ccttcaaagg c 51

<210> 13
 <211> 36
 <212> DNA
 <213> Homo sapiens

<400> 13
 ctcgaaccgg gctatagcag cacctgggtcc gtaaatt 36

<210> 14
 <211> 394
 <212> DNA
 <213> Homo sapiens

<400> 14
 caaatgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccgggggagtc tctgaagatc 60
 tcctgtaggg gttctggata cagggtttacc agctactgga tcaactgggt gcgccagctg 120
 cccgggaaag gcctagagtg gatgggcagg attgatccta ctgactctta taccaactac 180
 agtccatcct tcaaaggcca cgtcaccgtc tcagctgaca agtccatcaa cactgcctac 240
 ctgcagtgga gcagcctgaa ggcctcggac accggcatgt attactgtgc gaggctcgaa 300
 ccgggctata gcagcacctg gtccgtaaatt tggggccagg gaaccctgggt caccgtctcc 360
 tcagcctcca ccaagggcc atcgggtcttc cccc 394

<210> 15
 <211> 333
 <212> DNA
 <213> Homo sapiens

<400> 15
 ctgcctgtgc tgactcagcc accctcgggtg tctggagccc ccaggcagag ggtcaccatc 60
 tcctgttctg gaaacagctc caacatcgga aataatgctg taaactggta ccagcagctc 120
 ccaggaaagg ctcccaaact cctcatctat tatgatgata aactgccctc aggggtctct 180
 gaccgattct ctgggtccag gtctggcacc tccgcctccc tggccatccg tgggctccag 240
 tctgaggatg aggctgatta ttactgtaca tcatgggatg acagcctgga tagtcaactg 300
 ttcggcggag ggaccaggct gaccgtccta ggt 333

<210> 16
 <211> 39
 <212> DNA
 <213> Homo sapiens

<400> 16
 tctggaaaca gctccaacat cggaataat gctgtaaac 39

<210> 17
<211> 21
<212> DNA
<213> Homo sapiens

<400> 17
tatgatgatac aactgccctc a 21

<210> 18
<211> 33
<212> DNA
<213> Homo sapiens

<400> 18
acatcatggg atgacagcct ggatagtcaa ctg 33

<210> 19
<211> 119
<212> PRT
<213> Mus sp.

<400> 19

Asp Val Gln Ile Gln Gln Pro Gly Thr Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Tyr
20 25 30

Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met His Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ser Arg Asn Tyr Gly Ser Gly Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Leu Thr Val Ser Ser
115

<210> 20
<211> 5
<212> PRT
<213> Mus sp.

<400> 20

Thr Tyr Trp Met His .
1 5.

<210> 21
<211> 17
<212> PRT
<213> Mus sp.

<400> 21

Glu Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Asn Gln Lys Phe Lys
1 5 10 15

Gly

<210> 22
<211> 10
<212> PRT
<213> Mus sp.

<400> 22

Asn Tyr Gly Ser Gly Tyr Tyr Phe Asp Tyr
1 5 10

<210> 23
<211> 124
<212> PRT
<213> Mus sp.

<400> 23

Asp Val Gln Ile Gln Gln Pro Gly Thr Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Tyr
20 25 30

Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met His Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ser Arg Asn Tyr Gly Ser Gly Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly

100

105

110

Thr Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro
 115 120

<210> 24
 <211> 106
 <212> PRT
 <213> Mus sp.

<400> 24

Gly Val Glu Met Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
 1 5 10 15

Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
 20 25 30

His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
 35 40 45

Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Thr Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Trp Thr
 85 90 95

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 25
 <211> 10
 <212> PRT
 <213> Mus sp.

<400> 25

Ser Ala Ser Ser Ser Val Ser Tyr Met His
 1 5 10

<210> 26
 <211> 7
 <212> PRT
 <213> Mus sp.

<400> 26

Asp Thr Ser Lys Leu Ala Ser
 1 5

<210> 27
 <211> 9
 <212> PRT
 <213> Mus sp.

<400> 27

Gln Gln Trp Ser Ser Asn Pro Trp Thr
 1 5

<210> 28
 <211> 110
 <212> PRT
 <213> Mus sp.

<400> 28

Gly Val Glu Met Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
 1 5 10 15

Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
 20 25 30

His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
 35 40 45

Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Thr Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Trp Thr
 85 90 95

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Leu Met Leu
 100 105 110

<210> 29
 <211> 357
 <212> DNA
 <213> Mus sp.

<400> 29

gacgtccaga tccagcagcc tgggactgag cttgtgaagc ctggggcttc agtgagactg	60
tcctgcaagg cttctggcta caccttcacc acctactgga tgcactgggt gaagcagagg	120
cctggacaag gccttgagtg gatcgagag attgatcctt ctgatagtta tactaactat	180
aatcaaaagt tcaagggcaa ggccacattg actgtagaca aatcctccag cacagcctac	240
atgcacctca gcagcctgac atctgaggac tctgcggtct attactgttc aagaaactac	300

ggtagtggct actactttga ctactggggc caaggcacca ctctcacagt ctctca 357

<210> 30
<211> 15
<212> DNA
<213> Mus sp.

<400> 30
acctactgga tgcac 15

<210> 31
<211> 51
<212> DNA
<213> Mus sp.

<400> 31
gagattgac cttctgatag ttatactaac tataatcaaa agttcaaggg c 51

<210> 32
<211> 30
<212> DNA
<213> Mus sp.

<400> 32
aactacggta gtggctacta ctttgactac 30

<210> 33
<211> 373
<212> DNA
<213> Mus sp.

<400> 33
gacgtccaga tccagcagcc tgggactgag cttgtgaagc ctggggcttc agtgagactg 60

tcctgcaagg cttctggcta caccttcacc acctactgga tgcactgggt gaagcagagg 120

cctggacaag gccttgagtg gatcggagag attgatcctt ctgatagtta tactaactat 180

aatcaaaagt tcaagggcaa ggccacattg actgtagaca aatcctccag cacagcctac 240

atgcacctca gcagcctgac atctgaggac tctgcgggtct attactgttc aagaaactac 300

ggtagtggct actactttga ctactggggc caaggcacca ctctcacagt ctctcagcc 360

aaaacaacac ccc 373

<210> 34
<211> 318
<212> DNA
<213> Mus sp.

<400> 34
ggcgttgaga tgacacagtc gccagcaatc atgtctgcat ctccagggga gaaggtcacc 60

atgacctgca gtgccagctc aagtgttaagt tacatgcaact ggtaccagca gaagtcaggc 120

acctcccca aaagatggat ttatgacaca tccaaactgg cttctggagt ccctgctcgc 180

ttcagtggca gtgggtctgg gacctcttac tctctcacia tcagcagcat ggagactgaa	240
gatgctgccca cttattactg ccagcagtgg agtagtaacc cgtggacggt cggtggaggc	300
accaaactgg aaatcaaa	318

<210> 35
 <211> 30
 <212> DNA
 <213> Mus sp.

<400> 35 agtgccagct caagtgtatg ttacatgcac	30
--	----

<210> 36
 <211> 21
 <212> DNA
 <213> Mus sp.

<400> 36 gacacatcca aactggcttc t	21
-------------------------------------	----

<210> 37
 <211> 27
 <212> DNA
 <213> Mus sp.

<400> 37 cagcagtggg gtagtaaccc gtggacg	27
---	----

<210> 38
 <211> 331
 <212> DNA
 <213> Mus sp.

<400> 38 ggcggttgaga tgacacagtc gccagcaatc atgtctgcat ctccagggga gaaggtcacc	60
atgacctgca gtgccagctc aagtgtatg tacatgcact ggtaccagca gaagtcaggc	120
acctccccca aaagatggat ttatgacaca tccaaactgg cttctggagt ccctgctcgc	180
ttcagtggca gtgggtctgg gacctcttac tctctcacia tcagcagcat ggagactgaa	240
gatgctgccca cttattactg ccagcagtgg agtagtaacc cgtggacggt cggtggaggc	300
accaaactgg aaatcaaag gctgatgctg c	331